

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/073,138A

Source: FW16

Date Processed by STIC: 8/31/05

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IFW16

RAW SEQUENCE LISTING

DATE: 08/31/2005

PATENT APPLICATION: US/10/073,138A

TIME: 16:57:51

Input Set : A:\US10073138.txt

Output Set: N:\CRF4\08312005\J073138A.raw

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3 <110> APPLICANT: ANDERSON, DARRELL R.
4   HANNA, NABIL
5   BRAMS, PETER
6   HEARD, CHERYL
8 <120> TITLE OF INVENTION: INDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
9   CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
10  CO-STIMULATORY ANTIGENS
12 <130> FILE REFERENCE: 37003-280705
14 <140> CURRENT APPLICATION NUMBER: 10/073138A
15 <141> CURRENT FILING DATE: 2002-02-13
17 <150> PRIOR APPLICATION NUMBER: PCT/US97/19906
18 <151> PRIOR FILING DATE: 1997-10-29
20 <150> PRIOR APPLICATION NUMBER: 08/746,361
21 <151> PRIOR FILING DATE: 1996-11-08
23 <150> PRIOR APPLICATION NUMBER: 08/487,550
24 <151> PRIOR FILING DATE: 1995-06-07
26 <160> NUMBER OF SEQ ID NOS: 6
28 <170> SOFTWARE: PatentIn Ver. 2.1
30 <210> SEQ ID NO: 1
31 <211> LENGTH: 705
32 <212> TYPE: DNA
33 <213> ORGANISM: Homo sapiens
35 <220> FEATURE:
36 <221> NAME/KEY: CDS
37 <222> LOCATION: (1)..(702)
39 <400> SEQUENCE: 1
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42   1           5           10           15
44 ggt gca cga tgt gcc tat gaa ctg act cag cca ccc tcg gtg tca gtg   96
45 Gly Ala Arg Cys Ala Tyr Glu Leu Thr Gln Pro Pro Ser Val Ser Val
46   20           25           30
48 tcc cca gga cag acg gcc agg atc acc tgt ggg gga gac aac agt aga   144
49 Ser Pro Gly Gln Thr Ala Arg Ile Thr Cys Gly Gly Asp Asn Ser Arg
50   35           40           45
52 aat gaa tat gtc cac tgg tac cag cag aag cca gcg cgg gcc cct ata   192
53 Asn Glu Tyr Val His Trp Tyr Gln Gln Lys Pro Ala Arg Ala Pro Ile
54   50           55           60
56 ctg gtc atc tat gat gat agt gac cgg ccc tca ggg atc cct gag cga   240
57 Leu Val Ile Tyr Asp Asp Ser Asp Arg Pro Ser Gly Ile Pro Glu Arg
58   65           70           75           80
60 ttc tct ggc tcc aaa tca ggg aac acc gcc acc ctg acc atc aac ggg   288
61 Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Thr Leu Thr Ile Asn Gly

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64 gtc gag gcc ggg gat gag gct gac tat tac tgt cag gtg tgg gac agg 336
65 Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Arg
66          100          105          110
68 gct agt gat cat ccg gtc ttc gga gga ggg acc cgg gtg acc gtc cta 384
69 Ala Ser Asp His Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu
70          115          120          125
72 ggt cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct 432
73 Gly Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser
74          130          135          140
76 gag gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac 480
77 Glu Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp
78 145          150          155          160
80 ttc tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc 528
81 Phe Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro
82          165          170          175
84 gtc aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac 576
85 Val Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn
86          180          185          190
88 aag tac gcg gcc agc agc tac ctg agc ctg acg cct gag cag tgg aag 624
89 Lys Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys
90          195          200          205
92 tcc cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg 672
93 Ser His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val
94          210          215          220
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97 Glu Lys Thr Val Ala Pro Thr Glu Cys Ser
98 225          230
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103 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
106 <220> FEATURE:
107 <221> NAME/KEY: CDS
108 <222> LOCATION: (1)..(1428)
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113 1          5          10          15
115 gtc ctg tcc cag gtg aag ctg cag cag tgg ggc gaa gga ctt ctg cag 96
116 Val Leu Ser Gln Val Lys Leu Gln Gln Trp Gly Glu Gly Leu Leu Gln
117          20          25          30
119 cct tcg gag acc ctg tcc cgc acc tgc gtt gtc tct ggt ggc tcc atc 144
120 Pro Ser Glu Thr Leu Ser Arg Thr Cys Val Val Ser Gly Gly Ser Ile
121          35          40          45
123 agc ggt tac tac tac tgg acc tgg atc cgc cag acc cca ggg agg gga 192
124 Ser Gly Tyr Tyr Tyr Trp Thr Trp Ile Arg Gln Thr Pro Gly Arg Gly
125          50          55          60
127 ctg gag tgg att ggc cat att tat ggt aat ggt gcg acc acc aac tac 240

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129	65					70					75					80	
131	aat	ccc	tcc	ctc	aag	agt	cga	gtc	acc	att	tca	aaa	gac	acg	tcc	aag	288
132	Asn	Pro	Ser	Leu	Lys	Ser	Arg	Val	Thr	Ile	Ser	Lys	Asp	Thr	Ser	Lys	
133					85					90					95		
135	aac	cag	ttc	ttc	ctg	aac	ttg	aat	tct	gtg	acc	gac	gcg	gac	acg	gcc	336
136	Asn	Gln	Phe	Phe	Leu	Asn	Leu	Asn	Ser	Val	Thr	Asp	Ala	Asp	Thr	Ala	
137				100					105					110			
139	gtc	tat	tac	tgt	gcg	aga	ggc	cct	cgc	cct	gat	tgc	aca	acc	att	tgt	384
140	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Pro	Arg	Pro	Asp	Cys	Thr	Thr	Ile	Cys	
141			115					120					125				
143	tat	ggc	ggc	tgg	gtc	gat	gtc	tgg	ggc	ccg	gga	gac	ctg	gtc	acc	gtc	432
144	Tyr	Gly	Gly	Trp	Val	Asp	Val	Trp	Gly	Pro	Gly	Asp	Leu	Val	Thr	Val	
145		130					135					140					
147	tcc	tca	gct	agc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	gca	ccc	tcc	480
148	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	
149	145					150					155					160	
151	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	ctg	gtc	aag	528
152	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	
153					165					170					175		
155	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	ggc	gcc	ctg	576
156	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	
157			180						185				190				
159	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	tca	gga	ctc	624
160	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	
161			195					200					205				
163	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	ttg	ggc	acc	672
164	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	
165		210					215					220					
167	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	acc	aag	gtg	720
168	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	
169	225					230					235					240	
171	gac	aag	aaa	gca	gag	ccc	aaa	tct	tgt	gac	aaa	act	cac	aca	tgc	cca	768
172	Asp	Lys	Lys	Ala	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	
173				245						250					255		
175	ccg	tgc	cca	gca	cct	gaa	ctc	ctg	ggg	gga	ccg	tca	gtc	ttc	ctc	ttc	816
176	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	
177			260						265					270			
179	ccc	cca	aaa	ccc	aag	gac	acc	ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	864
180	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	
181			275					280					285				
183	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	912
184	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	
185		290					295					300					
187	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	960
188	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	
189	305					310					315					320	
191	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	1008
192	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	

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195 gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc 1056
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197          340          345          350
199 tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc 1104
200 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
201          355          360          365
203 aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg 1152
204 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
205          370          375          380
207 gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc 1200
208 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
209 385          390          395          400
211 ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg 1248
212 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
213          405          410          415
215 gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc 1296
216 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
217          420          425          430
219 ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag 1344
220 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
221          435          440          445
223 ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac 1392
224 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
225          450          455          460
227 tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga 1431
228 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
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233 <211> LENGTH: 720
234 <212> TYPE: DNA
235 <213> ORGANISM: Homo sapiens
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238 <221> NAME/KEY: CDS
239 <222> LOCATION: (1)..(717)
241 <400> SEQUENCE: 3
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243 Met Ser Leu Pro Ala Gln Leu Leu Gly Leu Leu Leu Cys Val Pro
244 1          5          10          15
246 ggg tcc agt ggg gaa gtt gtg atg act cag tct cca ctg tcc ctt ccc 96
247 Gly Ser Ser Gly Glu Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
248          20          25          30
250 atc aca cct gga gag ccg gcc tcc atc tcc tgt agg tct agt caa agc 144
251 Ile Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
252          35          40          45
254 ctt aaa cac agt aat gga gac acc ttc ctg agt tgg tat cag cag aag 192
255 Leu Lys His Ser Asn Gly Asp Thr Phe Leu Ser Trp Tyr Gln Gln Lys
256          50          55          60
258 cca ggc caa cct cca agg ctc ctg att tat aag gtt tct aac cgg gac 240

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259 Pro Gly Gln Pro Pro Arg Leu Leu Ile Tyr Lys Val Ser Asn Arg Asp
260 65 70 75 80
262 tct ggg gtc cca gac aga ttc agc ggc agt ggg gca ggg aca gat ttc 288
263 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ala Gly Thr Asp Phe
264 85 90 95
266 aca ctg aaa atc agc gca gtg gag gct gaa gat gtt ggg gtt tat ttc 336
267 Thr Leu Lys Ile Ser Ala Val Glu Ala Glu Asp Val Gly Val Tyr Phe
268 100 105 110
270 tgc ggg caa ggt aca agg act cct ccc act ttc ggc gga ggg acc aag 384
271 Cys Gly Gln Gly Thr Arg Thr Pro Thr Phe Gly Gly Thr Lys
272 115 120 125
274 gtg gaa atc aaa cgt acg gtg gct gca cca tct gtc ttc atc ttc ccg 432
275 Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
276 130 135 140
278 cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
279 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
280 145 150 155 160
282 ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
283 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
284 165 170 175
286 aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
287 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
288 180 185 190
290 agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
291 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
292 195 200 205
294 gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
295 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
296 210 215 220
298 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tga 720
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312 <400> SEQUENCE: 4
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315 1 5 10 15
317 gtc cag tgt gag gtg caa ctg gtg gag tct ggg gga ggc ttg gtc cag 96
318 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln
319 20 25 30
321 cct ggc ggg tcc ctg aga gtc tcc tgt gca gtc tct gga ttc acc ttc 144
322 Pro Gly Gly Ser Leu Arg Val Ser Cys Ala Val Ser Gly Phe Thr Phe
323 35 40 45

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